

The Reduced Genomes of Parcubacteria (OD1) Contain Signatures of a Symbiotic Lifestyle

Objective

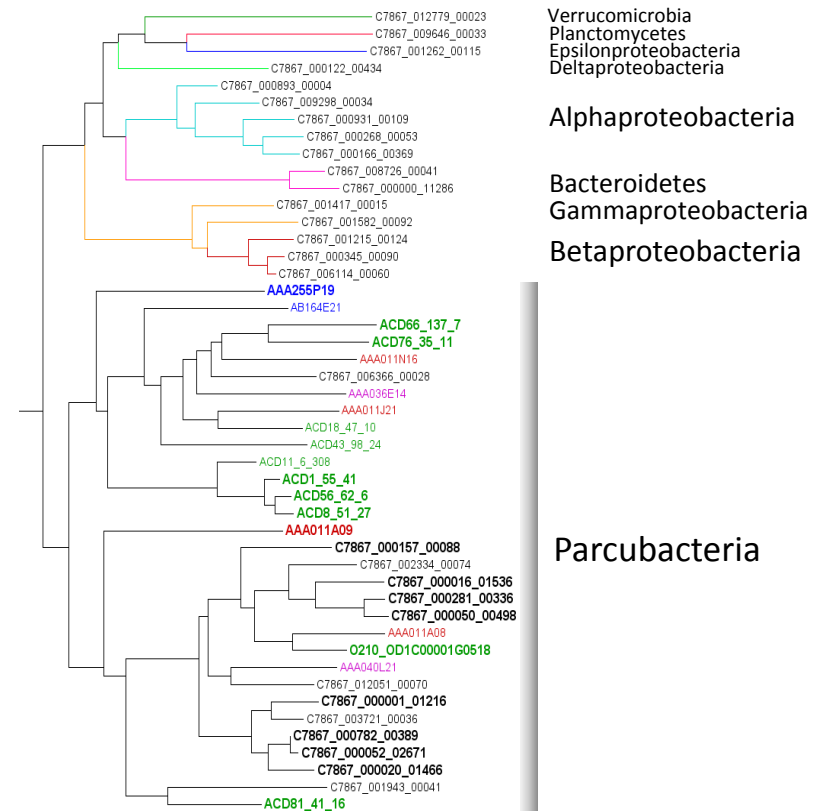
- Investigate the functionality and role of parclubacterial organisms, previously found exclusively in anaerobic environments, in Hanford oxic groundwater.

Approach and Results

- Eight near-complete genome sequences were reconstructed from a metagenomic data set derived from groundwater microbes.
- Genomes are small (0.5-1.2Mb) and lack ability to synthesize central metabolites such as amino acids, nucleotides and vitamins. They contain no TCA cycle and only the non-oxidative branch of the pentose-phosphate pathway.
- Parclubacterial genomes lack certain genes that were previously considered universally conserved, such as signal recognition particle, pseudouridine synthase RluA and riboflavin kinase/FAD synthase.
- Pan-genome analysis indicates a broad genotypic diversity and perhaps a highly fluid gene complement, indicating historical adaptation to a wide range of growth environments and a high degree of specialization.

Significance and Impact

- Genomic features such as the lack of biosynthetic capabilities, over-represented DNA repair machinery, and conserved attachment and adhesion genes suggest the Parclubacteria have a symbiotic/parasitic lifestyle.
- Other candidate phyla appear to have similar genomic properties, and thus bacterial symbiosis/parasitism may be more widespread than previously thought.



Nelson, W.C. and Stegen, J.C. (2015) The reduced genomes of Parclubacteria (OD1) contain signatures of a symbiotic lifestyle. *Front. Microbiol.* **6**, 713; doi: 10.3389/fmicb.2015.00713